

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/516, 813
Source: PCT
Date Processed by STIC: 12/14/2005

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/576, 813

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | |
|----------|---|
| 1 _____ | Wrapped Nucleics
Amino Acids
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." |
| 2 _____ | Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 _____ | Misaligned Amino
Numbering The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead. |
| 4 _____ | Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 _____ | Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 _____ | PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 _____ | Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |
| 8 _____ | Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional , please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 _____ | Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents. |
| 10 _____ | Invalid <213>
 Response <u>Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence</u> |
| 11 _____ | Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) |
| 12 _____ | PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. |
| 13 _____ | Misuse of n/Xaa " n " can only represent a single <u>nucleotide</u> ; " Xaa " can only represent a single <u>amino acid</u> |



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/516,813

DATE: 12/14/2005

TIME: 14:50:36

Input Set : A:\11752-007US1.txt

Output Set: N:\CRF4\12142005\J516813.raw

5 <110> APPLICANT: FRASER, JOHN D.
 8 <120> TITLE OF INVENTION: IMMUNOMODULATORY CONSTRUCTS AND THEIR USES
 11 <130> FILE REFERENCE: 11752-007US1
 14 <140> CURRENT APPLICATION NUMBER: US 10/516,813
 15 <141> CURRENT FILING DATE: 2004-12-03
 18 <150> PRIOR APPLICATION NUMBER: NZ 519371
 19 <151> PRIOR FILING DATE: 2002-06-04
 21 <150> PRIOR APPLICATION NUMBER: PCT/NZ03/00111
 22 <151> PRIOR FILING DATE: 2003-06-04
 25 <160> NUMBER OF SEQ ID NOS: 13
 28 <170> SOFTWARE: PatentIn version 3.1
 31 <210> SEQ ID NO: 1
 33 <211> LENGTH: 209
 35 <212> TYPE: PRT
 37 <213> ORGANISM: Streptococcus pyogenes
 40 <400> SEQUENCE: 1
 42 Leu Glu Val Asp Asn Asn Ser Leu Leu Arg Asn Ile Tyr Ser Thr Ile
 43 1 5 10 15
 46 Val Tyr Glu Tyr Ser Asp Ile Val Ile Asp Phe Lys Thr Ser His Asn
 47 20 25 30
 50 Leu Val Thr Lys Lys Leu Asp Val Arg Asp Ala Arg Asp Phe Phe Ile
 51 35 40 45
 54 Asn Ser Glu Met Asp Glu Tyr Ala Ala Asn Asp Phe Lys Thr Gly Asp
 55 50 55 60
 58 Lys Ile Ala Val Phe Ser Val Pro Phe Asp Trp Asn Tyr Leu Ser Lys
 59 65 70 75 80
 62 Gly Lys Val Thr Ala Tyr Thr Tyr Gly Gly Ile Thr Pro Tyr Gln Lys
 63 85 90 95
 66 Thr Ser Ile Pro Lys Asn Ile Pro Val Asn Leu Trp Ile Asn Gly Lys
 67 100 105 110
 70 Gln Ile Ser Val Pro Tyr Asn Glu Ile Ser Thr Asn Lys Thr Thr Val
 71 115 120 125
 74 Thr Ala Gln Glu Ile Asp Leu Lys Val Arg Lys Phe Leu Ile Ala Gln
 75 130 135 140
 78 His Gln Leu Tyr Ser Ser Gly Ser Ser Tyr Lys Ser Gly Arg Leu Val
 79 145 150 155 160
 82 Phe His Thr Asn Asp Asn Ser Asp Lys Tyr Ser Phe Asp Leu Phe Tyr
 83 165 170 175
 86 Val Gly Tyr Arg Asp Lys Glu Ser Ile Phe Lys Val Tyr Lys Asp Asn
 87 180 185 190
 90 Lys Ser Phe Asn Ile Asp Lys Ile Gly His Leu Asp Ile Glu Ile Asp
 91 195 200 205
 94 Ser

Does Not Comply
Corrected Diskette Needed

(pg-3,4)

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98 <210> SEQ ID NO: 2
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102 <212> TYPE: PRT
104 <213> ORGANISM: Streptococcus pyogenes
108 <400> SEQUENCE: 2
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111 1 5 10 15
114 Val Tyr Glu Tyr Ser Asp Ile Val Ile Asp Phe Lys Thr Ser His Cys
115 20 25 30
118 Leu Val Thr Lys Lys Leu Asp Val Arg Asp Ala Arg Asp Phe Phe Ile
119 35 40 45
122 Asn Ser Glu Met Asp Glu Tyr Ala Ala Asn Asp Phe Lys Thr Gly Asp
123 50 55 60
126 Lys Ile Ala Val Phe Ser Val Pro Phe Asp Trp Asn Tyr Leu Ser Lys
127 65 70 75 80
130 Gly Lys Val Thr Ala Tyr Thr Tyr Gly Gly Ile Thr Pro Tyr Gln Lys
131 85 90 95
134 Thr Ser Ile Pro Lys Asn Ile Pro Val Asn Leu Trp Ile Asn Gly Lys
135 100 105 110
138 Gln Ile Ser Val Pro Tyr Asn Glu Ile Ser Thr Asn Lys Thr Thr Val
139 115 120 125
142 Thr Ala Gln Glu Ile Asp Leu Lys Val Arg Lys Phe Leu Ile Ala Gln
143 130 135 140
146 His Gln Leu Tyr Ser Ser Gly Ser Ser Tyr Lys Ser Gly Arg Leu Val
147 145 150 155 160
150 Phe His Thr Asn Asp Asn Ser Asp Lys Tyr Ser Phe Asp Leu Leu Tyr
151 165 170 175
154 Val Gly Tyr Arg Asp Gln Glu Ser Ile Phe Lys Val Tyr Lys Asp Asn
155 180 185 190
158 Lys Ser Phe Asn Ile Asp Lys Ile Gly His Leu Asp Ile Glu Ile Asp
159 195 200 205
162 Ser
166 <210> SEQ ID NO: 3
168 <211> LENGTH: 209
170 <212> TYPE: PRT
172 <213> ORGANISM: Streptococcus pyogenes
176 <400> SEQUENCE: 3
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179 1 5 10 15
182 Val Ala Glu Tyr Ser Asp Ile Val Ile Asp Phe Lys Thr Ser His Cys
183 20 25 30
186 Leu Val Thr Lys Lys Leu Asp Val Arg Asp Ala Arg Asp Phe Phe Ile
187 35 40 45
190 Asn Ser Glu Met Asp Glu Tyr Ala Ala Asn Asp Phe Lys Thr Gly Asp
191 50 55 60
194 Lys Ile Ala Val Phe Ser Val Pro Phe Asp Trp Asn Tyr Leu Ser Lys
195 65 70 75 80
198 Gly Lys Val Thr Ala Tyr Thr Tyr Gly Gly Ile Thr Pro Tyr Gln Lys
199 85 90 95

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Output Set: N:\CRF4\12142005\J516813.raw

202 Thr Ser Ile Pro Lys Asn Ile Pro Val Asn Leu Trp Ile Asn Gly Lys
 203 100 105 110
 206 Gln Ile Ser Val Pro Tyr Asn Glu Ile Ser Thr Asn Lys Thr Thr Val
 207 115 120 125
 210 Thr Ala Gln Glu Ile Asp Leu Lys Val Arg Lys Phe Leu Ile Ala Gln
 211 130 135 140
 214 His Gln Leu Tyr Ser Ser Gly Ser Ser Tyr Lys Ser Gly Arg Leu Val
 215 145 150 155 160
 218 Phe His Thr Asn Asp Asn Ser Asp Lys Tyr Ser Phe Asp Leu Leu Tyr
 219 165 170 175
 222 Val Gly Tyr Arg Asp Gln Glu Ser Ile Phe Lys Val Tyr Lys Asp Asn
 223 180 185 190
 226 Lys Ser Phe Asn Ile Asp Lys Ile Gly His Leu Asp Ile Glu Ile Asp
 227 195 200 205
 230 Ser
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 236 <211> LENGTH: 27
 238 <212> TYPE: DNA
 240 <213> ORGANISM: Primer
 243 <400> SEQUENCE: 4
 244 cgattgtagc tgaattattca gatatag
 247 <210> SEQ ID NO: 5
 249 <211> LENGTH: 27
 251 <212> TYPE: DNA
 253 <213> ORGANISM: PRIMER
 256 <400> SEQUENCE: 5
 257 gaattattcag ctacaatcgt actatag
 260 <210> SEQ ID NO: 6
 262 <211> LENGTH: 24
 264 <212> TYPE: DNA
 266 <213> ORGANISM: PRIMER
 269 <400> SEQUENCE: 6
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 273 <210> SEQ ID NO: 7
 275 <211> LENGTH: 26
 277 <212> TYPE: DNA
 279 <213> ORGANISM: PRIMER
 282 <400> SEQUENCE: 7
 283 ctctagcaca tctaactca agtttc
 286 <210> SEQ ID NO: 8
 288 <211> LENGTH: 23
 290 <212> TYPE: DNA
 292 <213> ORGANISM: PRIMER
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 299 <210> SEQ ID NO: 9
 301 <211> LENGTH: 23
 303 <212> TYPE: DNA
 305 <213> ORGANISM: PRIMER

Invalid Respsns
 2137 Respsns
 Can be either
 Artificial, Unknown
 or Genus Species.
 P/s see glen # 10
 on error summary
 sheet.

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DATE: 12/14/2005

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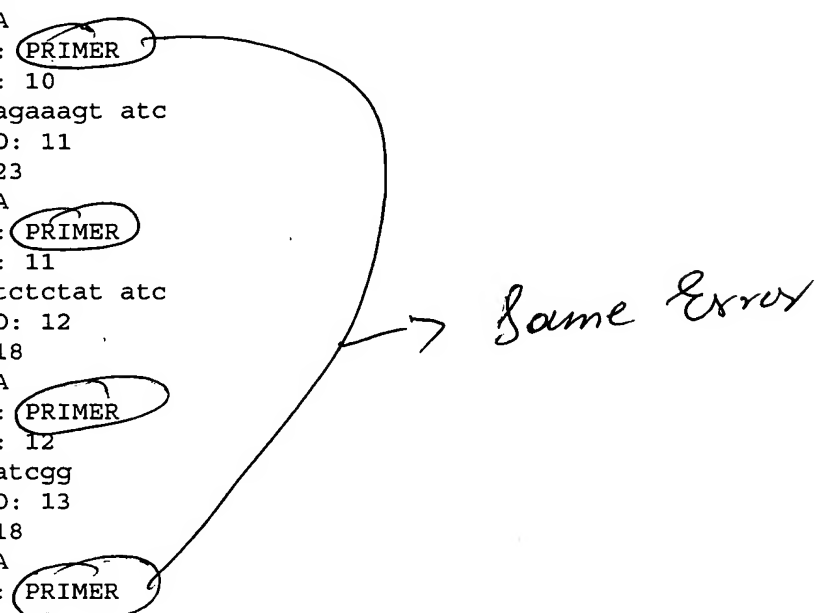
TIME: 14:50:36

Input Set : A:\11752-007US1.txt

Output Set: N:\CRF4\12142005\J516813.raw

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312 <210> SEQ ID NO: 10
314 <211> LENGTH: 23
316 <212> TYPE: DNA
318 <213> ORGANISM: PRIMER
321 <400> SEQUENCE: 10
322 gatatagaga tcaagaaagt atc 23
325 <210> SEQ ID NO: 11
327 <211> LENGTH: 23
329 <212> TYPE: DNA
331 <213> ORGANISM: PRIMER
335 <400> SEQUENCE: 11
336 gatactttct tgatctctat atc 23
339 <210> SEQ ID NO: 12
341 <211> LENGTH: 18
343 <212> TYPE: DNA
345 <213> ORGANISM: PRIMER
348 <400> SEQUENCE: 12
349 accatcctcc aaaatcgg 18
352 <210> SEQ ID NO: 13
354 <211> LENGTH: 18
356 <212> TYPE: DNA
358 <213> ORGANISM: PRIMER
361 <400> SEQUENCE: 13
362 tcagaggttt tcaccgtc 18

Same Error



VERIFICATION SUMMARY

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